

10/540092

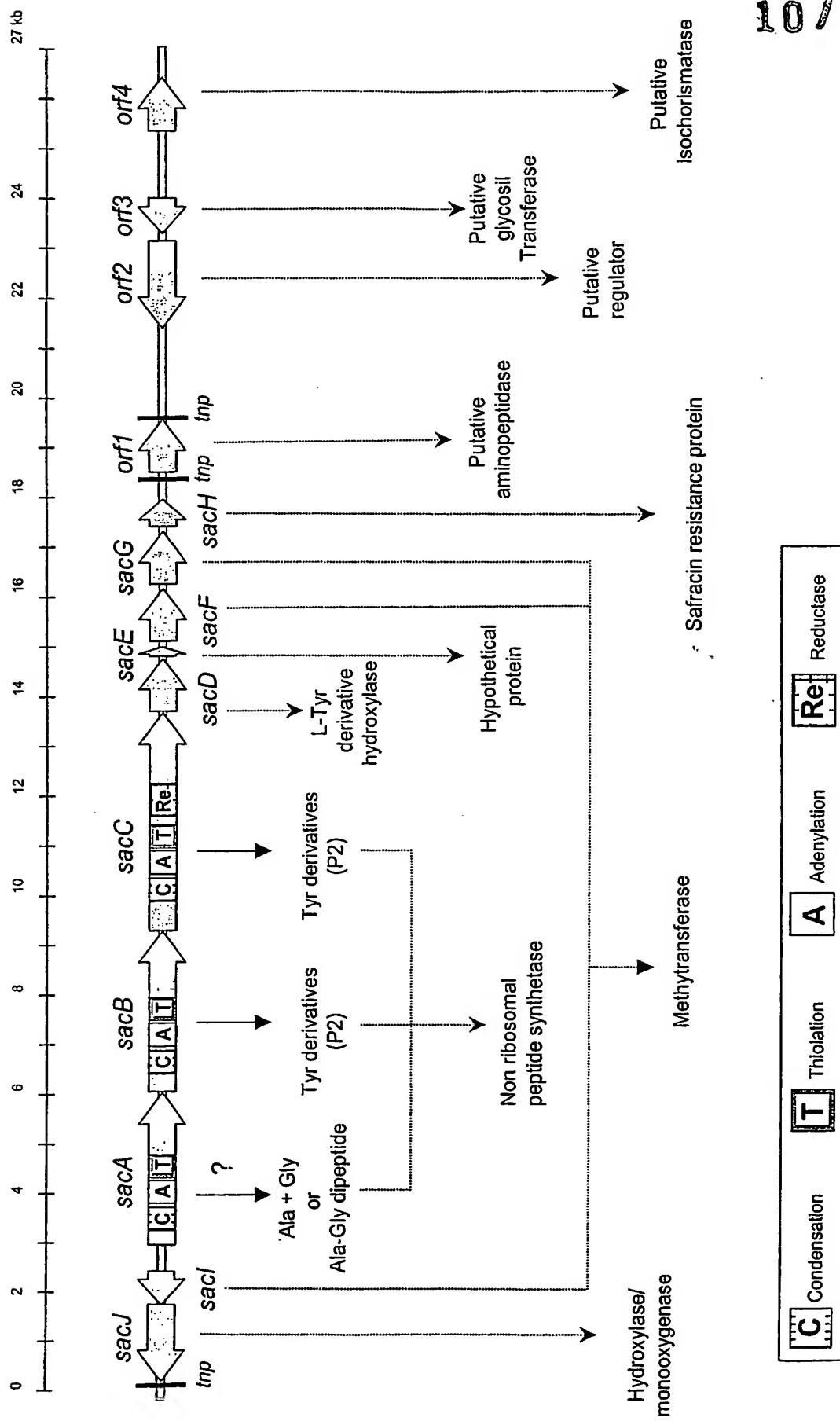


Figure 1

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Core	1	2	3	4	5	6
Sequence	LKAGGA	SGTTG	GELCGG	TGD	RIELGEIE	LGGHIS
SafB1	97	-LYAGVVAWPVYP-78-YTSGSTADPKG-220-GEIWRGSPSVAQGY-23-LRTGDL-23-NYPQDLEL-163-LPDLGLDSALVELKHRIE-				
SafB2	1247	-LEAGGVAVPLDP-64-YTSGSTGQPKG-172-GEFIGGAGVARGY-24-YRTGDL-23-FRIFEEIE-121-FFDLGGNSLLATRLATRLA-				
SafA1	559	-LKAGGAYVPLDP-64-YTSGSSGRPKG-173-GEFIGGSGVARGY-24-YRTGDL-23-YRIELAEIE-121-FFELGGNSLLAGRIVEELD-				
SafA2	1668	-LKAGGAYVPLDP-67-YTSGSTGTPKA-179-GEFIGVGGVLARGY-24-YRTGDL-23-YRVELGEIE-122-FFEVGGTSLLARLASRLL-				
SacA	483	-MACGGSYVPLSD-63-FTSGSTGEPKG-172-GEIILIGHGVAQGY-20-YRTGDR-23-FRVELGPVQ-121-FLDIGGHSLSLTHLTGLLR-				
SacB	524	-WQVGGIYVPLSK-63-YTSGSTGKPKG-173-GEILLICGPVVSQGY-22-YLTGDR-23-HRIELGEIE-123-FFQLGGHSILVARMVERIE-				
SacC	515	-RAGHAFLPIDPR-62-YTSGSTGVPKG-178-GEIMILAGONLARGY-21-YATGDL-23-HRIELNEVA-122-FFEQGGNSILLTRIACTLS-				
FUNCTION	unknown	ATP binding	ATP binding	ATPase	ATP binding	4' phosphopantetheine binding

Figure 2

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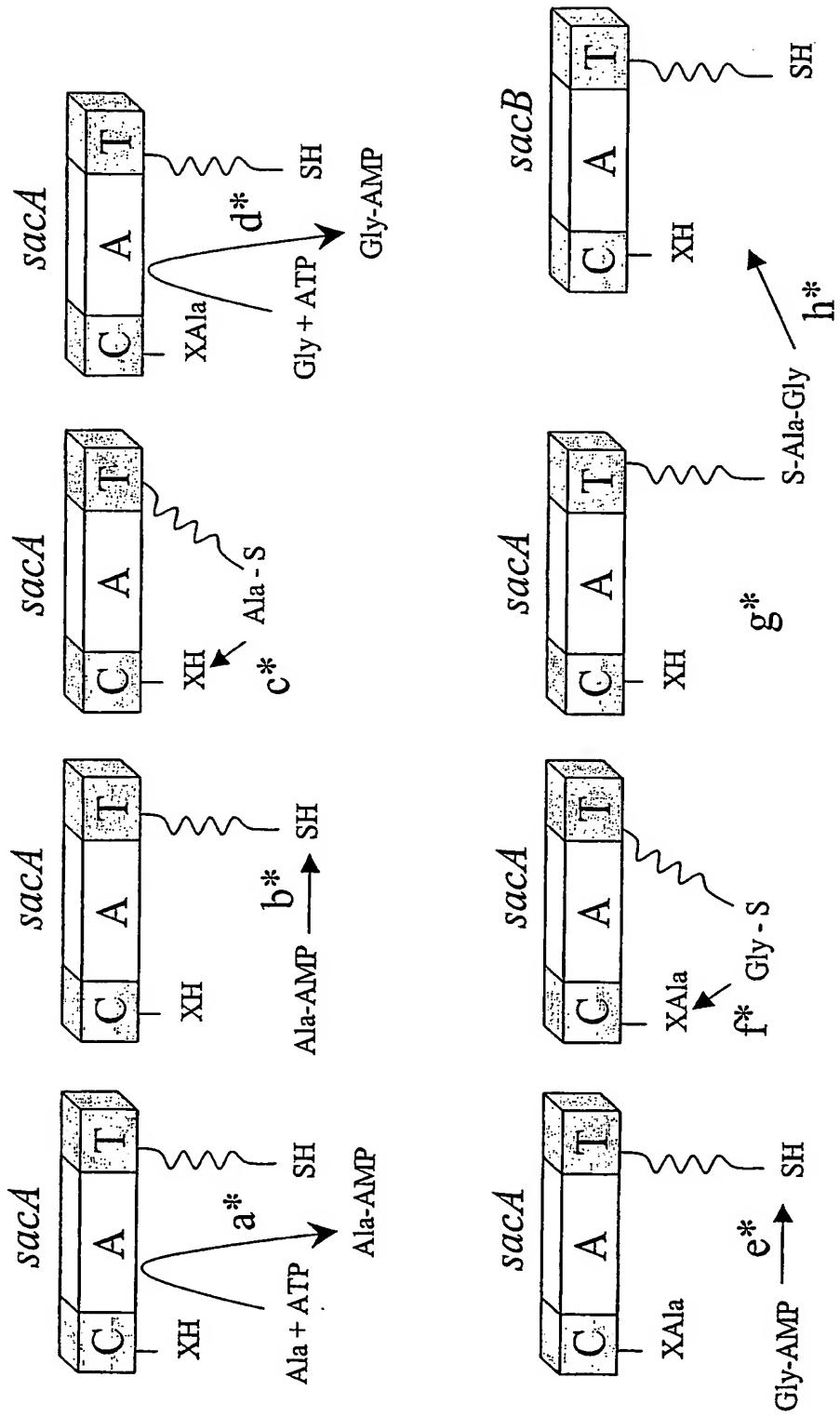


Figure 3

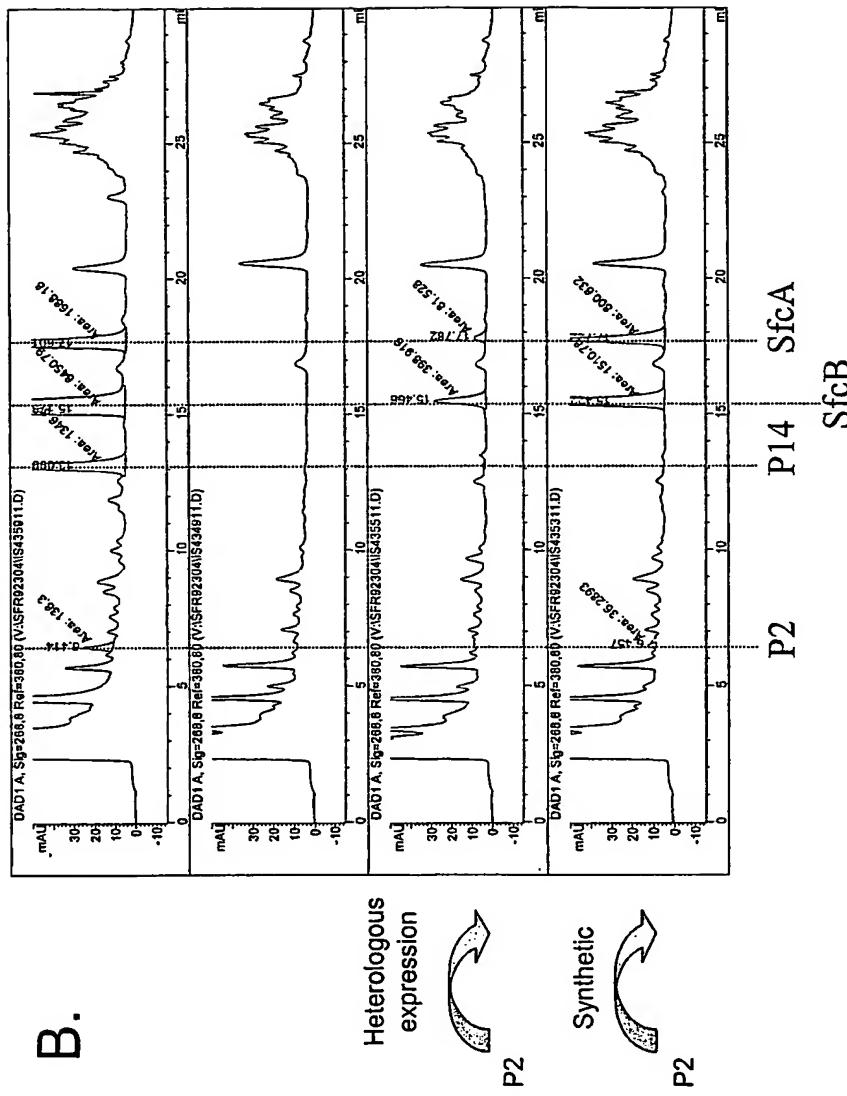
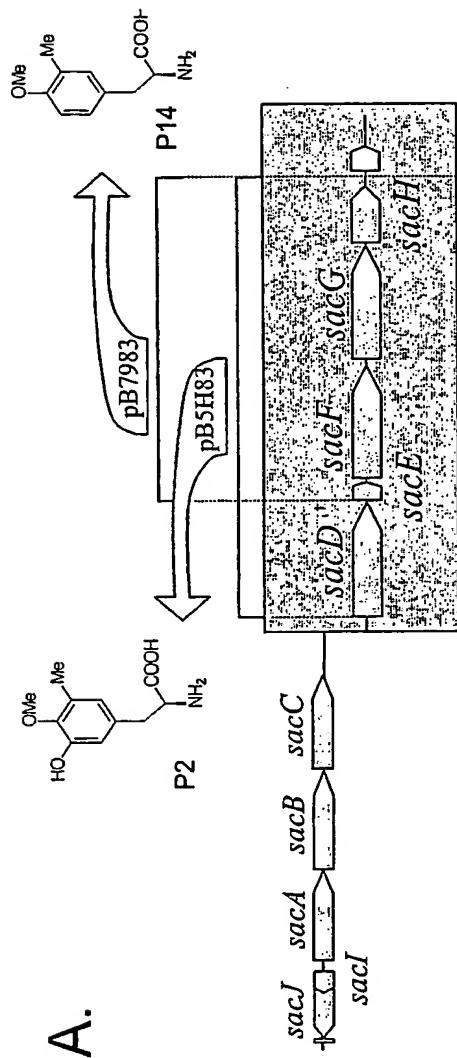


Figure 4

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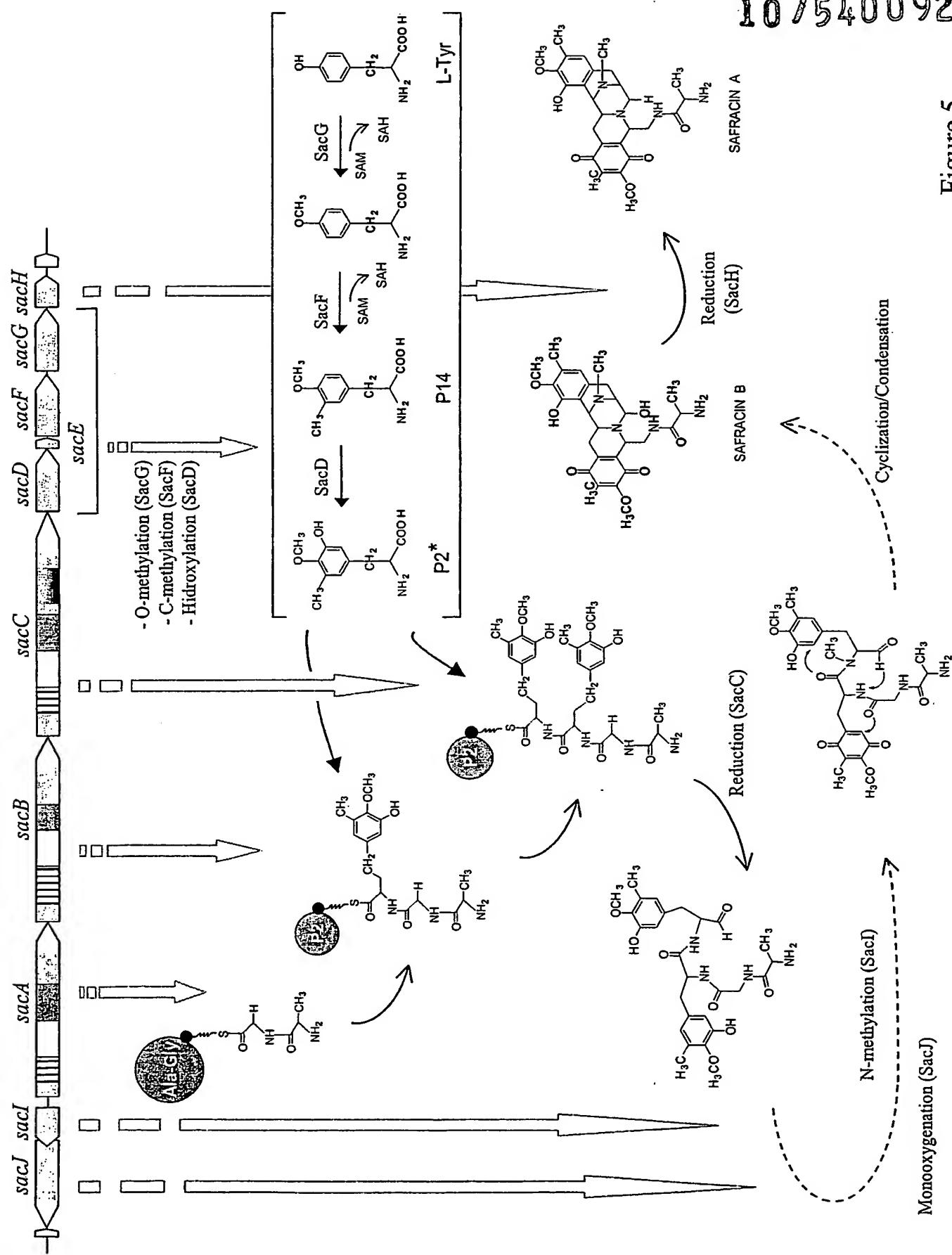


Figure 5

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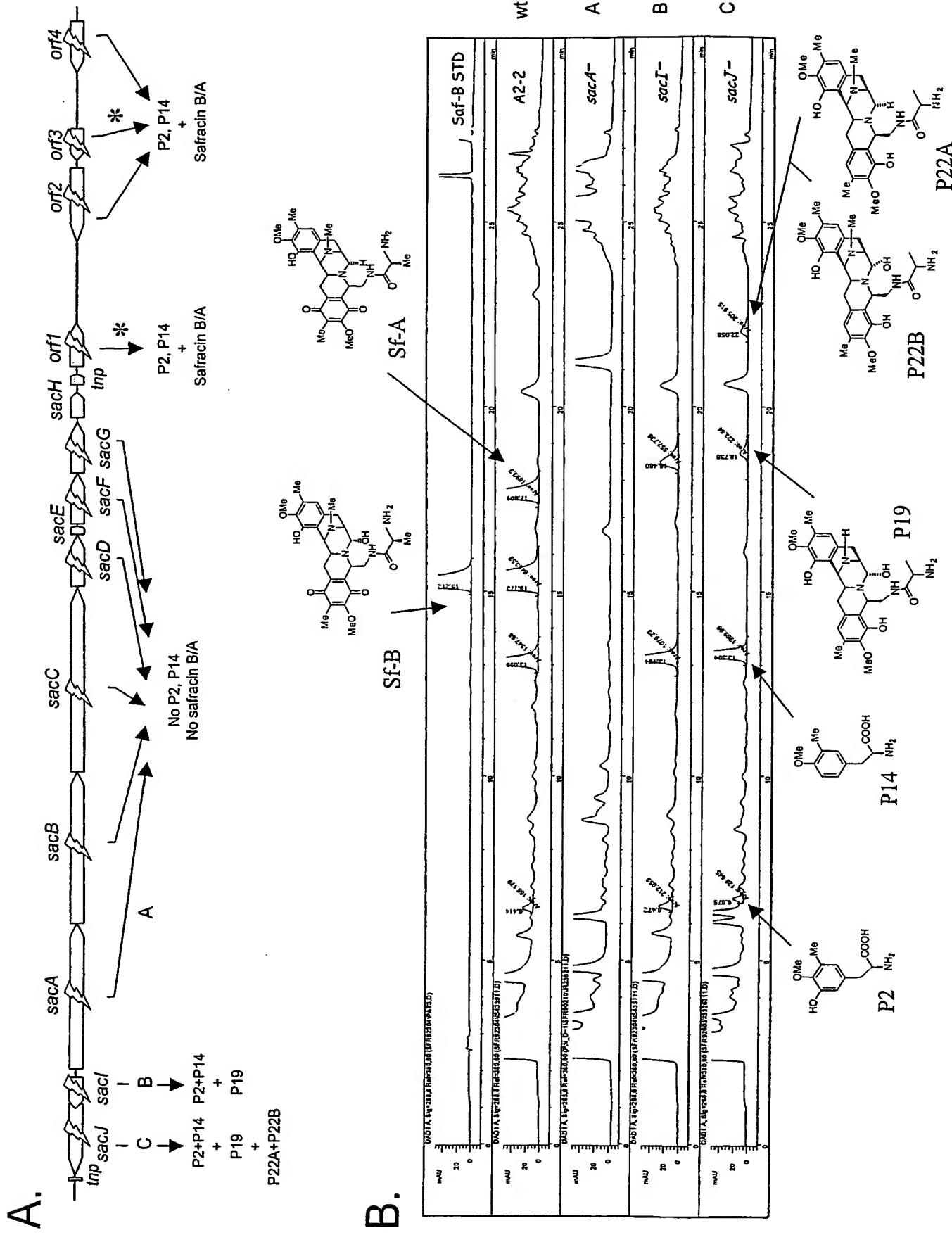


Figure 6

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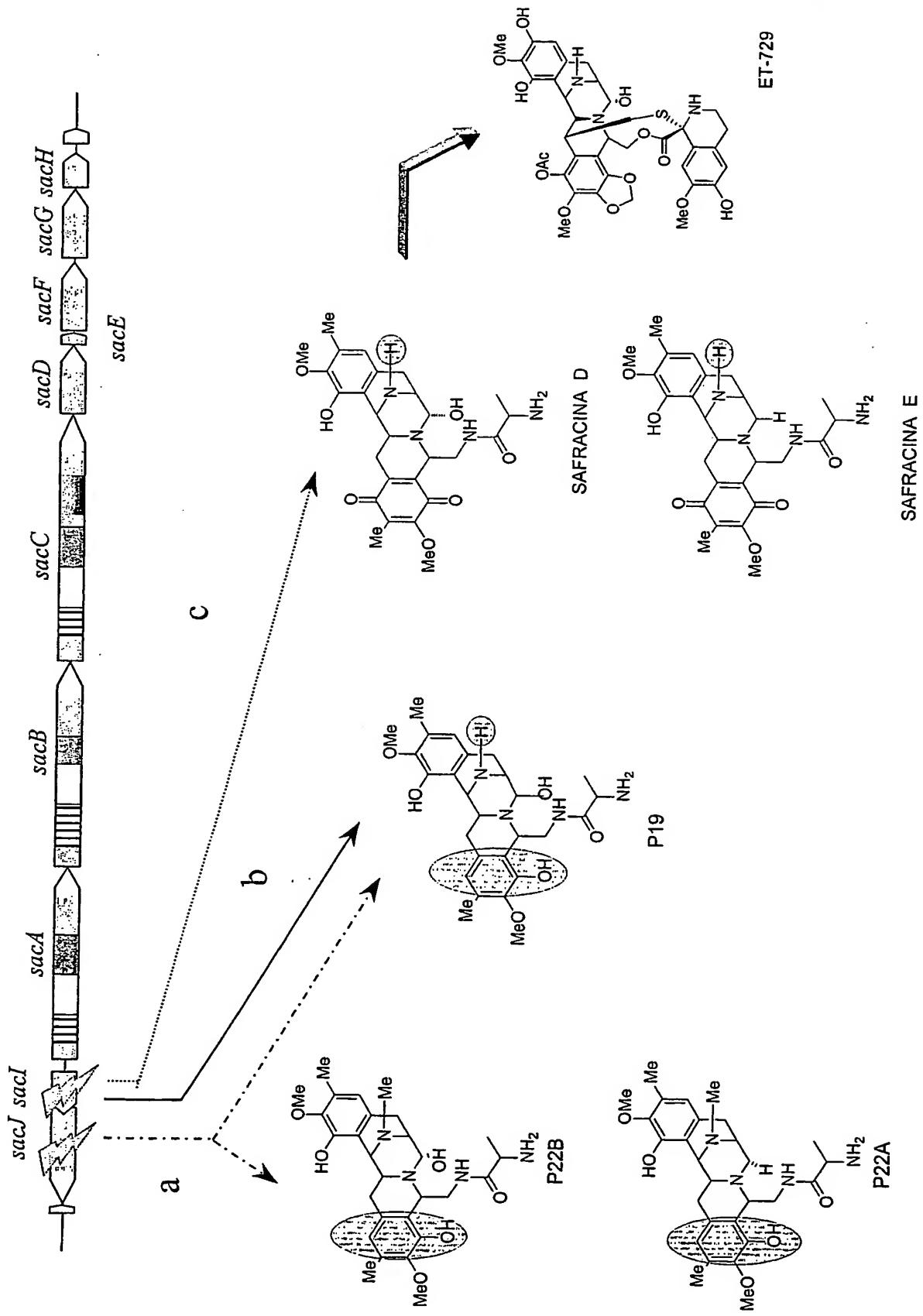


Figure 7

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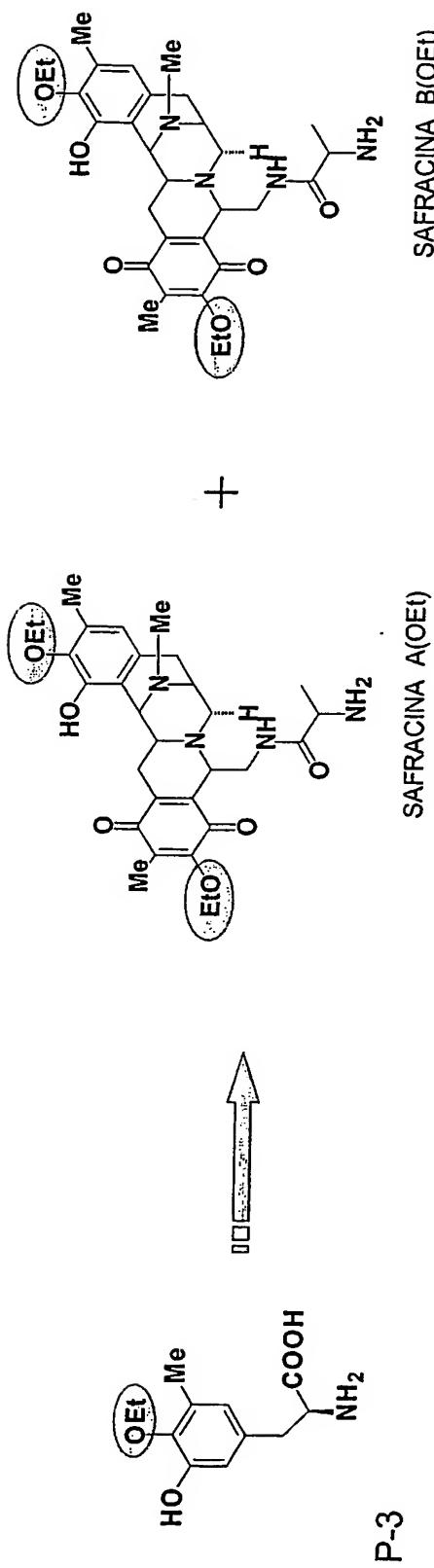


Figure 8

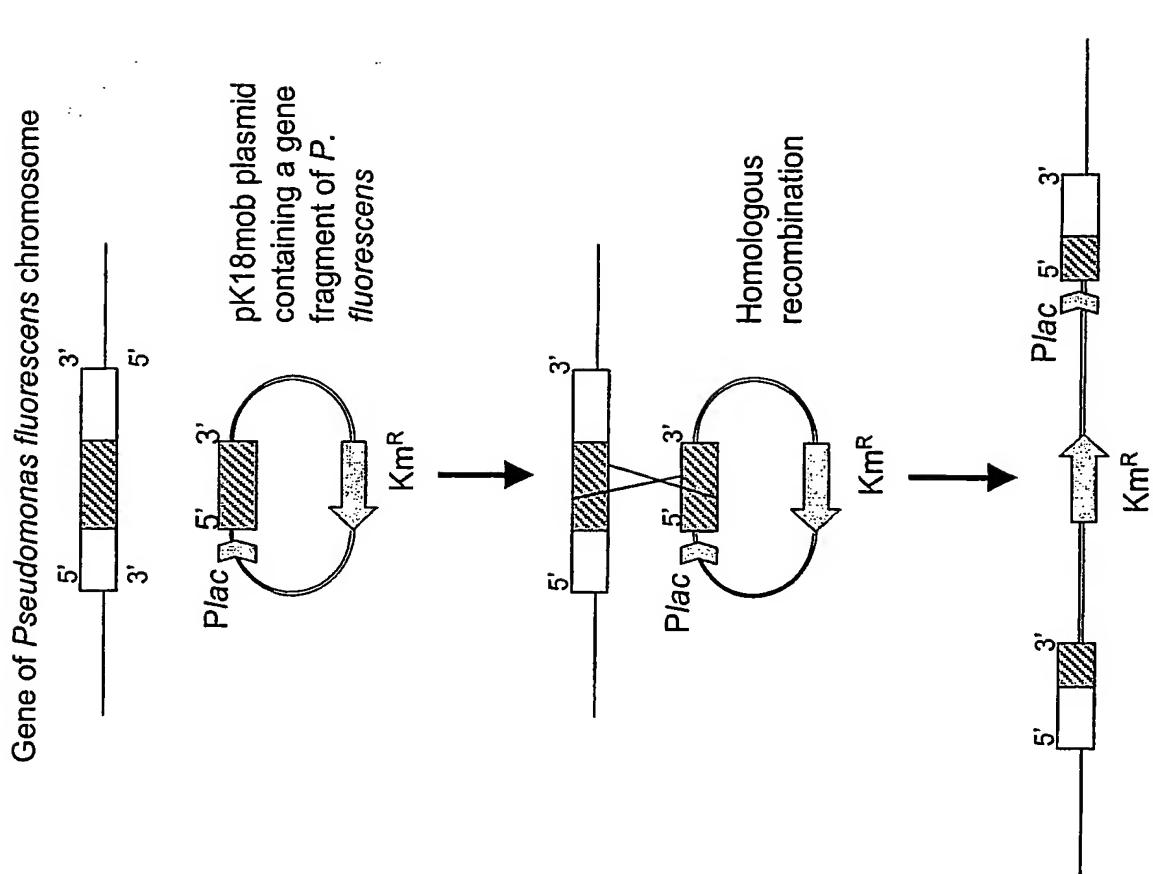


Figure 9